Figure 4a

```
sp|P00737|HPT1_HUMAN   MSALGAVIALLLWGQLFAVDSGNDVTDIADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRT  60
sp|P00738|HPT2_HUMAN   MSALGAVIALLLWGQLFAVDSGNDVTDIADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRT  60
sp|P50417|HPT_ATEGE    MSALGAVIALLLWGQLFAVDSGNDVTDIADDGCPKPPEIANGYVEHLVRYQCKKYYRLRT  60
tr|Q60574|Q60574       MRALGAVVTLLLWGQLFAVELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRA  60
tr|Q61646|Q61646       MRALGAVVTLLLWGQLFAVELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRA  60
sp|Q62558|HPT_MUSSA    MRALGAVVTLLLWGQLFAAELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRT  60
sp|P06866|HPT_RAT      MRALGAVVTLLLWGQLFAVELGNDATDIEDDSCPKPPEIANGYVEHLVRYRCRQFYKLQT  60
tr|O35086|O35086       MRALGAVVTLLLWGQLFAVDLSNDAMDTADDSCPKPPEIENGYVEHLVRYRC-QHYRLRT  59
sp|P19006|HPT_CANFA    -----------------EDTGSEATNNTEVSLPKPPVIENGYVEHMIRYQCKPFYKLHT  42
                                        : ..:. :   :  . **** * :***** :**:*  .*:*::


sp|P00737|HPT1_HUMAN   EGDGVYTLN---------------------------------------------------  69
sp|P00738|HPT2_HUMAN   EGDGVYTLNDKKQWINKAVGDKLPECEADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRTE 120
sp|P50417|HPT_ATEGE    EGDGVYTLN---------------------------------------------------  69
tr|Q60574|Q60574       EGDGVYTLN---------------------------------------------------  69
tr|Q61646|Q61646       EGDGVYTLN---------------------------------------------------  69
sp|Q62558|HPT_MUSSA    EGDGVYTLN---------------------------------------------------  69
sp|P06866|HPT_RAT      EGDGIYTLN---------------------------------------------------  69
tr|O35086|O35086       EGDGVYTLN---------------------------------------------------  68
sp|P19006|HPT_CANFA    EGDGVYTLN---------------------------------------------------  51
                       ****:****


sp|P00737|HPT1_HUMAN   --------NEKQWINKAVGDKLPECEAVCGKPKNPANPVQRILGGHLDAKGSFPWQAKMV 121
sp|P00738|HPT2_HUMAN   GDGVYTLNNEKQWINKAVGDKLPECEAVCGKPKNPANPVQRILGGHLDAKGSFPWQAKMV 180
sp|P50417|HPT_ATEGE    --------NEKQWTNKAVGDKLPECEAVCGKPKNPANPVQRILGGHLDAKGSFPWQAKMV 121
tr|Q60574|Q60574       --------DEKQWMNTVAGEKLPECEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI 121
tr|Q61646|Q61646       --------DEKQWVNTVAGEKLPECEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI 121
sp|Q62558|HPT_MUSSA    --------DEKQWVNTAAGEKLPECEAVCGKPKHPVVQVQRIIGGSMDAKGSFPWQAKMI 121
sp|P06866|HPT_RAT      --------SEKQWVNPAAGDKLPKCEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI 121
tr|O35086|O35086       --------SEKQWVNTAAGERLPECEAVCGKPKHPVDQVQRIIGGSLDAKGSFPWQAKMV 120
sp|P19006|HPT_CANFA    --------SEKHWTNKAVGEKLPECEAVCGKPKNPVDQVQRIMGGSVDAKGSFPWQAKMV 103
                               .**:* *  ..*::**:**********:*.   ****:** :***********:


sp|P00737|HPT1_HUMAN   SHHNLTTGATLINEQWLLTTAKNLFLNHSENATAKDIAPTLTLYVGKKQLVEIEKVVLHP 181
sp|P00738|HPT2_HUMAN   SHHNLTTGATLINEQWLLTTAKNLFLNHSENATAKDIAPTLTLYVGKKQLVEIEKVVLHP 240
sp|P50417|HPT_ATEGE    SRHNLTTGATLINEQWLLTTAKNLFLNHSENATAKDIAPTLTLYVGKNQLVEIEKVVLYP 181
tr|Q60574|Q60574       SRHGLTTGATLISDQWLLTTAKNLFLNHSETASGKDIAPTLTLYVGKNQLVEIEKVILHP 181
tr|Q61646|Q61646       SRHGLTTGATLISDQWLLTTAKNLFLNHSETASAKDITPTLTLYVGKNQLVEIEKVVLHP 181
sp|Q62558|HPT_MUSSA    SRHGLTTGATLISDQWLLTTAKNLFLNHSETASAKDIAPTLTLYVGKNQLVEIEKVVLHP 181
sp|P06866|HPT_RAT      SRHGLTTGATLISDQWLLTTAQNLFLNHSENATAKDIAPTLTLYVGKNQLVEIEKVVLHP 181
tr|O35086|O35086       SRHELITGATLISDQWLLTTAKNLFLNHSEDATSKDIAPTLKLYVGKMQPVEIEKVVIHP 180
sp|P19006|HPT_CANFA    SHHNLTSGATLINEQWLLTTAKNLFLGHKDDAKANDIAPTLKLYVGKNQLVEVEKVVLHP 163
                       *:* *  :*****.:*******:****.*.:  *  .:**:***.***** * **:***::*


sp|P00737|HPT1_HUMAN   NYSQVDIGLIKLKQKVSVNERVMPICLPSKDYAEVGRVGYVSGWGRNANFKFTDHLKYVM 241
sp|P00738|HPT2_HUMAN   NYSQVDIGLIKLKQKVSVNERVMPICLPSKDYAEVGRVGYVSGWGRNANFKFTDHLKYVM 300
sp|P50417|HPT_ATEGE    NYSQVDIGLIKLKDKVPVNERVMPICLPSKDYAEVGRVGYVSGWGRNANFKFTDHLKYVM 241
tr|Q60574|Q60574       NHSVVDIGLIKLKQRVLVTERVMPICLPSKDYVAPGRVGYVSGWGRNQDFRFTDRLKYVM 241
tr|Q61646|Q61646       NHSVVDIGLIKLKQRVLVTERVMPICLPSKDYIAPGRVGYVSGWGRNANFRFTDRLKYVM 241
sp|Q62558|HPT_MUSSA    NHSVVDIGLIKLKQRVLVTERVMPICLPSKDYVAPGRVGYLSGWGRNVNFRFTERFKYVM 241
sp|P06866|HPT_RAT      ERSVVDIGLIKLKQKVLVTEKVMPICLPSKDYVAPGRMGYVSGWGRNVNFRFTERLKYVM 241
tr|O35086|O35086       NRSVVDIGVIKLKQKVPVNERVMPICLPSKDYIAPGRMGYVSGWGRNANFRFTDRLKYVM 240
sp|P19006|HPT_CANFA    DYSKVDIGLIKLKQKVPIDERVMPICLPSKDYAEVGRIGYVSGWGRNSNFNFTELLKYVM 223
                       : *  ****:***::* :  *:*********** **::****** :*.**: :****


sp|P00737|HPT1_HUMAN   LPVADQDQCIRHYEGSTVPEKKTPKSPVGVQPILNEHTFCAGMSKYQEDTCYGDAGSAFA 301
sp|P00738|HPT2_HUMAN   LPVADQDQCIRHYEGSTVPEKKTPKSPVGVQPILNEHTFCAGMSKYQEDTCYGDAGSAFA 360
sp|P50417|HPT_ATEGE    LPVADQYQCVKHYEGSTVPEKKTPKSPVGQQPILNEHTFCAGMSKYQEDTCYGDAGSAFA 301
tr|Q60574|Q60574       LPVADQDKCVVHYEKSTVPEKKNFTSPVGVQPILNEHTFCAGLTKYEEDTCYGDAGSAFA 301
tr|Q61646|Q61646       LPVADQDKCVVHYENSTVPEKKNLTSPVGVQPILNEHTFCVGLTKYEEDTCYGDAGSAFA 301
sp|Q62558|HPT_MUSSA    LPVADQDKCVVHYENSTVPEKKNFTSPVGVQPILNEHTFCVGLSRYQEDTCYGDAGSAFA 301
sp|P06866|HPT_RAT      LPVADQEKCELHYEKSTVPEKKGAVTPVGVQPILNKHTFCAGLTKYEEDTCYGDAGSAFA 301
tr|O35086|O35086       LPVADQDSCMLHYEGSTVPEKEGSKSSVGVQPILNEHTFCAGMTKYQEDTCYGDAGSAFA 300
sp|P19006|HPT_CANFA    LPVADQDKCVQHYEGSTVPEKKSPKSPVGVQPILNEHTFCAGMSKFQEDTCYGDAGSAFA 283
                       ****** .*  *** ******:     :.** *****:****.*::::::*************
```

Figure 4b

```
sp|P00737|HPT1_HUMAN    VHDLEEDTWYATGILSFDKSCAVAEYGVYVKVTSIQDWVQKTIAEN 347
sp|P00738|HPT2_HUMAN    VHDLEEDTWYATGILSFDKSCAVAEYGVYVKVTSIQDWVQKTIAEN 406
sp|P50417|HPT_ATEGE     VHDLEEDTWYAAGILSFDKSCGVAEYGVYVKATSIQDWVQKTIAEN 347
tr|Q60574|Q60574        IHDMEEDTWYAAGILSFDKSCAVAEYGVYVRATDLKDWVQETMAKN 347
tr|Q61646|Q61646        IHDMEEDTWYAAGILSFDKSCAVAEYGVYVRATDLKDWVQETMAKN 347
sp|Q62558|HPT_MUSSA     IHDMEEDTWXAAGILSFDKSCAVAEYGVYVRATDLKDWVQETMAKK 347
sp|P06866|HPT_RAT       VHDTEEDTWYAAGILSFDKSCAVAEYGVYVKATDLKDWVQETMAKN 347
tr|O35086|O35086        IHDLEQDTWYAAGILSFDKSCSVAEYGVYVKVNSFLDWIQETMAKN 346
sp|P19006|HPT_CANFA     VHDQDEDTWYAAGILSFDKSCTVAEYGVYVKVPSVLAWVQETIAGN 329
                        :**  ::*** *:********* *******:.  ..  *:*:*:* :
```

```
CD163                  MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDKELRLVDGENKCSGRVE 60
CD163 cyt. Var 1       MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDKELRLVDGENKCSGRVE 60
CD163 cyt. var 2       MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDKELRLVDGENKCSGRVE 60
CD163 ext. cell. Var.  MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDKELRLVDGENKCSGRVE 60
                       ************************************************************

tr|Q07898|Q07898       VKVQEEWGTVCNNGWSMEAVSVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNES 120
tr|Q07901|Q07901       VKVQEEWGTVCNNGWSMEAVSVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNES 120
tr|Q07900|Q07900       VKVQEEWGTVCNNGWSMEAVSVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNES 120
tr|Q07899|Q07899       VKVQEEWGTVCNNGWSMEAVSVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNES 120
                       ************************************************************

tr|Q07898|Q07898       ALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIEIKFQGRWGTVCD 180
tr|Q07901|Q07901       ALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIEIKFQGRWGTVCD 180
tr|Q07900|Q07900       ALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIEIKFQGRWGTVCD 180
tr|Q07899|Q07899       ALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIEIKFQGRWGTVCD 180
                       ************************************************************

tr|Q07898|Q07898       DNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWFDDLICNGNESALWNCKHQGWGK 240
tr|Q07901|Q07901       DNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWFDDLICNGNESALWNCKHQGWGK 240
tr|Q07900|Q07900       DNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWFDDLICNGNESALWNCKHQGWGK 240
tr|Q07899|Q07899       DNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWFDDLICNGNESALWNCKHQGWGK 240
                       ************************************************************

tr|Q07898|Q07898       HNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK 300
tr|Q07901|Q07901       HNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK 300
tr|Q07900|Q07900       HNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK 300
tr|Q07899|Q07899       HNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK 300
                       ************************************************************

tr|Q07898|Q07898       QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHEWGKHYCNHNEDAGVTC 360
tr|Q07901|Q07901       QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHEWGKHYCNHNEDAGVTC 360
tr|Q07900|Q07900       QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHEWGKHYCNHNEDAGVTC 360
tr|Q07899|Q07899       QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHEWGKHYCNHNEDAGVTC 360
                       ************************************************************

tr|Q07898|Q07898       SDGSDLELRLRGGGSRCAGTVEVEIQRLLGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ 420
tr|Q07901|Q07901       SDGSDLELRLRGGGSRCAGTVEVEIQRLLGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ 420
tr|Q07900|Q07900       SDGSDLELRLRGGGSRCAGTVEVEIQRLLGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ 420
tr|Q07899|Q07899       SDGSDLELRLRGGGSRCAGTVEVEIQRLLGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ 420
                       ************************************************************

tr|Q07898|Q07898       VYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLVGGDI 480
tr|Q07901|Q07901       VYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLVGGDI 480
tr|Q07900|Q07900       VYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLVGGDI 480
tr|Q07899|Q07899       VYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLVGGDI 480
                       ************************************************************

tr|Q07898|Q07898       PCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVVSILGGAHFGEGNGQIWAEEF 540
tr|Q07901|Q07901       PCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVVSILGGAHFGEGNGQIWAEEF 540
tr|Q07900|Q07900       PCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVVSILGGAHFGEGNGQIWAEEF 540
tr|Q07899|Q07899       PCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVVSILGGAHFGEGNGQIWAEEF 540
                       ************************************************************

tr|Q07898|Q07898       QCEGHESHLSLCPVAPRPEGTCSHSRDVGVVCS--------------------------- 573
tr|Q07901|Q07901       QCEGHESHLSLCPVAPRPEGTCSHSRDVGVVCSSKTQKTSLIGSYTVKGTGLGSHSCLFL 600
tr|Q07900|Q07900       QCEGHESHLSLCPVAPRPEGTCSHSRDVGVVCS--------------------------- 573
tr|Q07899|Q07899       QCEGHESHLSLCPVAPRPEGTCSHSRDVGVVCS--------------------------- 573
                       ********************************

tr|Q07898|Q07898       ------RYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST 627
tr|Q07901|Q07901       KPCLLPGYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST 660
tr|Q07900|Q07900       ------RYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST 627
tr|Q07899|Q07899       ------RYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST 627
                       *********************************************************
```